LISTING OF CLAIMS

None of the claims is amended in this response. However, for the convenience of the Applicants and the Examiner, a complete listing of the claims in their current format is provided below.

1. (Previously Presented) A method of identifying a sequence of a nucleic acid for use as a substrate surface immobilized probe for a target nucleic acid, said method comprising:

(a) determining via an algorithm a full length synthesis probability measure for each member sequence of a set of a plurality of candidate probe sequences for said target nucleic acid by determining the susceptibility to depurination during synthesis of each probe sequence; and

(b) employing said determined full length synthesis probability measures to identify and select a sequence for use as a substrate immobilized probe for said target nucleic acid.

2. (Original) The method according to Claim 1, wherein those sequences of said set that satisfy a full length synthesis probability threshold are selected.

3. (Original) The method according to Claim 2, wherein said full length synthesis probability measure is a measure of the probability that said candidate probe sequence will be fully synthesized by an in situ nucleic acid synthesis protocol.

4. (Original) The method according to Claim 3, wherein said full length synthesis probability measure is an evaluation of said candidate probe sequence's depurination susceptibility during said in situ nucleic acid synthesis protocol.

5. (Original) The method according to Claim 4, wherein said depurination susceptibility measure is a deblock dose or parameter based thereon.

6. (Original) The method according to Claim 5, wherein said method comprises determining a total deblock dose for each member sequence of said set.

7. (Original) The method according to Claim 6, wherein said full length synthesis probability threshold is a total deblock dose threshold and selected sequences have a total deblock dose that does not exceed said deblock dose threshold.

8. (Original) The method according to Claim 6, wherein said total deblock dose is a sum of individual deblock doses over all A nucleotides of said candidate probe sequence, except for any 5' terminal A nucleotide.

9. (Original) The method according to Claim 8, wherein each of said individual deblock doses d(x) for an A nucleotide positioned at layer x of a candidate probe sequence to be produced by a process having L total layers is equal to L-x+1.

10. (Original) The method according to Claim 1, wherein at least some of said steps are carried out by a computational analysis system.

Claims 11 and 12 (Cancelled).

13. (Original) A method of producing a nucleic acid array, said method comprising:

producing at least two different probe nucleic acids immobilized on a surface of a solid support, wherein at least one of said at least two different probe nucleic acids has a sequence of nucleotides identified according to the method of Claim 1.

14. (Original) The method according to Claim 13, wherein said at least two different probe nucleic acids are produced on said surface of said solid support by synthesizing said probe nucleic acids on said surface.

15. (Original) The method according to Claim 13, wherein said at least two different probe nucleic acids are produced on said surface of said solid support by depositing said at least two different probe nucleic acids onto said surface of said solid support.

Claims 16-21 (Cancelled).

22. (Previously Presented) In a method of identifying a sequence of a nucleic acid that is suitable for use as a substrate surface immobilized probe for a target nucleic acid, the improvement comprising:

determining depurination susceptibility for a plurality of candidate probe sequences for said target nucleic acid.

23. (Cancelled).

24. (Previously Presented) A method of identifying a sequence of a nucleic acid for use as a substrate surface immobilized probe for a target nucleic acid, said method comprising:

(a) determining a full length synthesis probability measure for each member sequence of a set of a plurality of candidate probe sequences for said target nucleic acid by determining the susceptibility to depurination during synthesis of each probe sequence; and

(b) employing said determined full length synthesis probability measures to identify and select a sequence for use as a substrate immobilized probe for said target nucleic acid.

25. (Previously Presented) The method according to Claim 24, wherein said depurination susceptibility measure is a deblock dose or parameter based thereon.

26. (Previously Presented) The method according to Claim 25, wherein said method comprises determining a total deblock dose for each member sequence of said set.

27. (Previously Presented) The method according to Claim 26, wherein said full length synthesis probability threshold is a total deblock dose threshold and selected sequences have a total deblock dose that does not exceed said deblock dose threshold.

28. (Previously Presented) The method according to Claim 26, wherein said total deblock dose is a sum of individual deblock doses over all A nucleotides of said candidate probe sequence, except for any 5' terminal A nucleotide.

29. (Previously Presented) The method according to Claim 28, wherein each of said individual deblock doses d(x) for an A nucleotide positioned at layer x of a candidate probe sequence to be produced by a process having L total layers is equal to L-x+1.

30. (Previously Presented) A method according to Claim 1, wherein said method further comprises synthesizing a nucleic acid having said selected sequence.

31. (Previously Presented) A method according to Claim 1, wherein said method further comprises outputting said full length synthesis probability measure to a user.